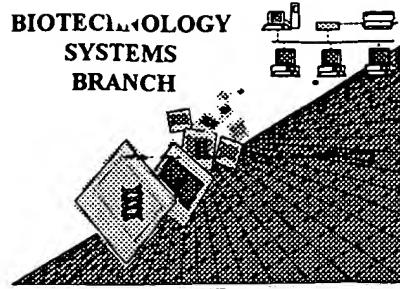


0270

BIOTECHNOLOGY
SYSTEMS
BRANCH



RAW SEQUENCE LISTING ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/679,687

Source: OIPE

Date Processed by STIC: 10/19/2000

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
 - 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY
- FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.

PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)

PATENTIN 3.0 e-mail help: patin30help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0

The Checker Version 3.0 application is a state-of the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 – 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO).

Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:
<http://www.uspto.gov/web/offices/pac/checker>

Raw Sequence Listing Error Summary

<u>ERROR DETECTED</u>	<u>SUGGESTED CORRECTION</u>	<u>SERIAL NUMBER:</u> <u>09/679,687</u>
ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE		
1 <input type="checkbox"/> Wrapped Nucleics	The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3, as this will prevent "wrapping".	
2 <input type="checkbox"/> Wrapped Aminos	The amino acid number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3, as this will prevent "wrapping".	
3 <input type="checkbox"/> Incorrect Line Length	The rules require that a line not exceed 72 characters in length. This includes spaces.	
4 <input type="checkbox"/> Misaligned Amino Acid Numbering	The numbering under each 5th amino acid is misaligned. This may be caused by the use of tabs between the numbering. It is recommended to delete any tabs and use spacing between the numbers.	
5 <input type="checkbox"/> Non-ASCII	This file was not saved in ASCII (DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text so that it can be processed.	
6 <input type="checkbox"/> Variable Length	Sequence(s) <input type="checkbox"/> contain n's or Xaa's which represented more than one residue. As per the rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the (ix) feature section that some may be missing.	
7 <input type="checkbox"/> PatentIn ver. 2.0 "bug"	A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequence(s) <input type="checkbox"/> . Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies primarily to the mandatory <220>-<223> sections for Artificial or Unknown sequences.	
8 <input type="checkbox"/> Skipped Sequences (OLD RULES)	Sequence(s) <input type="checkbox"/> missing. If intentional, please use the following format for each skipped sequence: (2) INFORMATION FOR SEQ ID NO:X: (i) SEQUENCE CHARACTERISTICS:(Do not insert any headings under "SEQUENCE CHARACTERISTICS") (xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: This sequence is intentionally skipped Please also adjust the "(iii) NUMBER OF SEQUENCES:" response to include the skipped sequence(s).	
9 <input type="checkbox"/> Skipped Sequences (NEW RULES)	Sequence(s) <input type="checkbox"/> missing. If intentional, please use the following format for each skipped sequence: <210> sequence id number <400> sequence id number 000	
10 <input checked="" type="checkbox"/> Use of n's or Xaa's (NEW RULES)	Use of n's and/or Xaa's have been detected in the Sequence Listing. Use of <220> to <223> is MANDATORY if n's or Xaa's are present. In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.	
11 <input type="checkbox"/> Use of <213>Organism (NEW RULES)	Sequence(s) <input type="checkbox"/> are missing this mandatory field or its response.	
12 <input type="checkbox"/> Use of <220>Feature (NEW RULES)	Sequence(s) <input type="checkbox"/> are missing the <220>Feature and associated headings. Use of <220> to <223> is MANDATORY if <213>ORGANISM is "Artificial" or "Unknown" Please explain source of genetic material in <220> to <223> section. (See "Federal Register," 6/01/98, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of new Rules)	
13 <input type="checkbox"/> PatentIn ver. 2.0 "bug"	Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other means to copy file to floppy disk.	

OIPE

RAW SEQUENCE LISTING DATE: 10/19/2000
 PATENT APPLICATION: US/09/679,687 TIME: 11:29:17

Input Set : A:\BB1162 US NA Seq Listing.txt
 Output Set: N:\CRF3\10192000\I679687.raw

3 <110> APPLICANT: Allen, Stephen M.
 4 Hitz, William D.
 5 Rafalski, J. Antoni
 7 <120> TITLE OF INVENTION: SUCROSE TRANSPORT PROTEINS
 9 <130> FILE REFERENCE: BB1162 US NA
 OK 11 <140> CURRENT APPLICATION NUMBER: US/09/679,687
 12 <141> CURRENT FILING DATE: 2000-10-05
 14 <150> PRIOR APPLICATION NUMBER: 60/081,148
 W--> 15 <151> PRIOR FILING DATE: April 9, 1998 → 1998-04-09
 17 <150> PRIOR APPLICATION NUMBER: PCT/US99/07562
 W--> 18 <151> PRIOR FILING DATE: April 7, 1999 → 1999-04-07
 OK 20 <160> NUMBER OF SEQ ID NOS: 28
 22 <170> SOFTWARE: Microsoft Office 97

ERRORED SEQUENCES

Does Not Comply
 Corrected Diskette Needed

use this date format
 when employing new
 Sequence Rule format

see following pages for more errors

09/679,687

2

<210> 19
<211> 2083
<212> DNA
<213> Triticum aestivum

<400> 19

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) see
item 10
in Error
summary
sheet

09/679,687

3

<210> 25

<211> 501

<212> PRT

<213> Daucus carota<400>

25Met Ala Gly Pro Glu Ala Asp Arg Asn Arg His Arg

Gly Gly Ala Thr 1

5

10

15

↑
Insert hard return

↓
Insert hard return

Ala Ala Pro Pro Arg Ser Arg Val Ser Leu Arg Leu Leu Arg

20

25

30

↑
Insert hard return

VERIFICATION SUMMARY DATE: 10/19/2000
PATENT APPLICATION: US/09/679,687 TIME: 11:29:18

Input Set : A:\BB1162 US NA Seq Listing.txt
Output Set: N:\CRF3\10192000\I679687.raw

L:11 M:270 C: Current Application Number differs, Replaced Application Number
L:12 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:15 M:256 W: Invalid Numeric Header Field, Wrong Prior FILING DATE:YYYY-MM-DD
L:18 M:256 W: Invalid Numeric Header Field, Wrong Prior FILING DATE:YYYY-MM-DD
L:826 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:13
L:826 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:13
L:900 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:14
L:900 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:14
L:903 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:14
M:340 Repeated in SeqNo=14
L:1062 M:258 W: Mandatory Feature missing, <220> not found for SEQ ID#:19
L:1062 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:19
L:1062 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:19
L:1062 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:19
L:1062 M:340 W: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:19
L:1587 M:280 W: Numeric Identifier already exists, Length not replaced.
L:1588 M:280 W: Numeric Identifier already exists, Type not replaced.
L:1589 M:280 W: Numeric Identifier already exists, Organism not replaced.
L:20 M:203 E: No. of Seq. differs, <160> Number Of Sequences:Input (28) Counted (27)